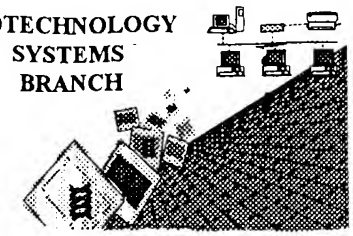
BIOTECHNOLOGY
SYSTEMS
BRANCH



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/070,241
Source: PCT/10
Date Processed by STIC: 9/12/2002

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO **REDUCE** ERRORED SEQUENCE LISTINGS, **PLEASE** USE THE **CHECKER VERSION 3.1 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
http://www.uspto.gov/web/offices/pac/checker

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<**http://www.uspto.gov/ebc/efs/downloads/documents.htm**> , **EFS Submission User Manual** - ePAVE)
2. **U.S. Postal Service:** U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. **Hand Carry directly to:**
   U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
   Or
   U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. **Federal Express, United Parcel Service, or other delivery service to:** U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 01/29/2002

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 10/020,241

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1	Wrapped Nucleics Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
2	Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.
3	Misaligned Amino Numbering	The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
4	Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
5	Variable Length	Sequence(s)____contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
6	PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
7	Skipped Sequences (OLD RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
8	Skipped Sequences (NEW RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000
9	Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
10	Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
11	Use of <220>	Sequence(s) 3-7 missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
12	PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
13	Misuse of n	n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

PCT10

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/070,241

DATE: 09/12/2002
TIME: 16:05:59

Input Set : A:\EP.txt
Output Set: N:\CRF4\09122002\J070241.raw

Does Not Comply
Corrected Diskette Needed

3 <110> APPLICANT: Takeda Chemical Industries, Ltd.
W--> 4 <120> TITLE OF INVENTION: Novel G Protein Coupled Receptor Protein and Its Use
W--> 5 <130> FILE REFERENCE: 2633WO0P
C--> 6 <140> CURRENT APPLICATION NUMBER: US/10/070,241
C--> 6 <141> CURRENT FILING DATE: 2000-08-24
6 <150> PRIOR APPLICATION NUMBER: JP 11-241530
7 <151> PRIOR FILING DATE: 1999-08-27
W--> 8 <160> NUMBER OF SEQ ID: 7
W--> 9 <210> SEQ ID NO: 1
10 <211> LENGTH: 431
11 <212> TYPE: PRT
12 <213> ORGANISM: Human
W--> 13 <400> SEQUENCE: 1

```
14 Met Gln Ala Leu Asn Ile Thr Pro Glu Gln Phe Ser Arg Leu Leu Arg
15  1               5                  10                  15
16 Asp His Asn Leu Thr Arg Glu Gln Phe Ile Ala Leu Tyr Arg Leu Arg
17             20                  25                  30
18 Pro Leu Val Tyr Thr Pro Glu Leu Pro Gly Arg Ala Lys Leu Ala Leu
19         35                  40                  45
20 Val Leu Thr Gly Val Leu Ile Phe Ala Leu Ala Leu Phe Gly Asn Ala
21     50                  55                  60
22 Leu Val Phe Tyr Val Val Thr Arg Ser Lys Ala Met Arg Thr Val Thr
23 65                  70                  75                  80
24 Asn Ile Phe Ile Cys Ser Leu Ala Leu Ser Asp Leu Leu Ile Thr Phe
25                 85                  90                  95
26 Phe Cys Ile Pro Val Thr Met Leu Gln Asn Ile Ser Asp Asn Trp Leu
27             100                 105                 110
28 Gly Gly Ala Phe Ile Cys Lys Met Val Pro Phe Val Gln Ser Thr Ala
29         115                 120                 125
30 Val Val Thr Glu Ile Leu Thr Met Thr Cys Ile Ala Val Glu Arg His
31     130                 135                 140
32 Gln Gly Leu Val His Pro Phe Lys Met Lys Trp Gln Tyr Thr Asn Arg
33 145                 150                 155                 160
34 Arg Ala Phe Thr Met Leu Gly Val Val Trp Leu Val Ala Val Ile Val
35                 165                 170                 175
36 Gly Ser Pro Met Trp His Val Gln Gln Leu Glu Ile Lys Tyr Asp Phe
37             180                 185                 190
38 Leu Tyr Glu Lys Glu His Ile Cys Cys Leu Glu Glu Trp Thr Ser Pro
39         195                 200                 205
40 Val His Gln Lys Ile Tyr Thr Thr Phe Ile Leu Val Ile Leu Phe Leu
41     210                 215                 220
42 Leu Pro Leu Met Val Met Leu Ile Leu Tyr Ser Lys Ile Gly Tyr Glu
43 225                 230                 235                 240
```

gpc 2-3

RAW SEQUENCE LISTING DATE: 09/12/2002
PATENT APPLICATION: **US/10/070,241** TIME: 16:05:59

Input Set : **A:\EP.txt**
Output Set: **N:\CRF4\09122002\J070241.raw**

```
Leu Trp Ile Lys Lys Arg Val Gly Asp Gly Ser Val Leu Arg Thr Ile
                245                 250                 255
His Gly Lys Glu Met Ser Lys Ile Ala Arg Lys Lys Lys Arg Ala Val
            260                 265                 270
Ile Met Met Val Thr Val Val Ala Leu Phe Ala Val Cys Trp Ala Pro
        275                 280                 285
Phe His Val Val His Met Met Ile Glu Tyr Ser Asn Phe Glu Lys Glu
    290                 295                 300
Tyr Asp Asp Val Thr Ile Lys Met Ile Phe Ala Ile Val Gln Ile Ile
305                 310                 315                 320
Gly Phe Ser Asn Ser Ile Cys Asn Pro Ile Val Tyr Ala Phe Met Asn
                325                 330                 335
Glu Asn Phe Lys Lys Asn Val Leu Ser Ala Val Cys Tyr Cys Ile Val
            340                 345                 350
Asn Lys Thr Phe Ser Pro Ala Gln Arg His Gly Asn Ser Gly Ile Thr
        355                 360                 365
Met Met Arg Lys Lys Ala Lys Phe Ser Leu Arg Glu Asn Pro Val Glu
    370                 375                 380
Glu Thr Lys Gly Glu Ala Phe Ser Asp Gly Asn Ile Glu Val Lys Leu
385                 390                 395                 400
Cys Glu Gln Thr Glu Glu Lys Lys Lys Leu Lys Arg His Leu Ala Leu
                405                 410                 415
Phe Arg Ser Glu Leu Ala Glu Asn Ser Pro Leu Asp Ser Gly His
            420                 425                 430
<210> SEQ ID NO: 2
<211> LENGTH: 1293
<212> TYPE: DNA
<213> ORGANISM: Human
W--> <400> SEQUENCE: 2
C--> atgcaggcgc ttaacattac cccggagcag ttctctcggc tgctgcggga ccacaacctg   60
     acgcgggagc agttcatcgc tctgtaccgg ctgcgaccgc tcgtctacac cccagagctg  120
     ccgggacgcg ccaagctggc cctcgtgctc accggcgtgc tcatcttcgc cctggcgctc  180
     tttggcaatg ctctggtgtt ctacgtggtg acccgcagca aggccatgcg caccgtcacc  240
     aacatcttta tctgctcctt ggcgctcagt gacctgctca tcaccttctt ctgcattccc  300
     gtcaccatgc tccagaacat ttccgacaac tggctggggg gtgctttcat ttgcaagatg  360
     gtgccatttg tccagtctac cgctgttgtg acagaaatcc tcactatgac ctgcattgct  420
     gtggaaaggc accagggact tgtgcatcct tttaaaatga agtggcaata caccaaccga  480
     agggctttca caatgctagg tgtggtctgg ctggtggcag tcatcgtagg atcacccatg  540
     tggcacgtgc aacaacttga gatcaaatat gacttcctat atgaaaagga acacatctgc  600
     tgcttagaag agtggaccag ccctgtgcac cagaagatct acaccacctt catccttgtc  660
     atcctcttcc tcctgcctct tatggtgatg cttattctgt acagtaaaat tggttatgaa  720
     ctttggataa agaaaagagt tggggatggt tcagtgcttc gaactattca tggaaaagaa  780
     atgtccaaaa tagccaggaa gaagaaacga gctgtcatta tgatggtgac agtggtggct  840
     ctctttgctg tgtgctgggc accattccat gttgtccata tgatgattga atacagtaat  900
     tttgaaaagg aatatgatga tgtcacaatc aagatgattt ttgctatcgt gcaaattatt  960
     ggattttcca actccatctg taatcccatt gtctatgcat ttatgaatga aaacttcaaa 1020
     aaaaatgttt tgtctgcagt ttgttattgc atagtaaata aaaccttctc tccagcacaa 1080
     aggcatggaa attcaggaat tacaatgatg cggaagaaag caaagttttc cctcagagag 1140
     aatccagtgg aggaaaccaa aggagaagca ttcagtgatg gcaacattga agtcaaattg 1200
```

all bases must be in lower-case letters, if Sequence Listing is in "new" Sequence Rules format

RAW SEQUENCE LISTING DATE: 09/12/2002
PATENT APPLICATION: US/10/070,241 TIME: 16:05:59

Input Set : A:\EP.txt
Output Set: N:\CRF4\09122002\J070241.raw

93 tgtgaacaga cagaggagaa gaaaaagctc aaacgacatc ttgctctctt taggtctgaa 1260
94 ctggctgaga attctccttt agacagtggg cat 1293
95 <210> SEQ ID NO: 3
96 <211> LENGTH: 37
97 <212> TYPE: DNA
98 <213> ORGANISM: Artificial Sequence
W--> 99 <220> FEATURE:
100 <223> OTHER INFORMATION: ← see item 11 on Error Summary Sheet
W--> 101 <400> SEQUENCE: 3
C--> 102 tgtcagcatg caggcgctta acattacccc ggagcag 37 ← use lower-case letters for bases
103 <210> SEQ ID NO: 4
104 <211> LENGTH: 37
105 <212> TYPE: DNA
106 <213> ORGANISM: Artificial Sequence
W--> 107 <220> FEATURE:
108 <223> OTHER INFORMATION: see item 11
W--> 109 <400> SEQUENCE: 4
C--> 110 gactagttta atgcccactg tctaaaggag aattctc 37
111 <210> SEQ ID NO: 5
112 <211> LENGTH: 22
113 <212> TYPE: DNA
114 <213> ORGANISM: Artificial Sequence
W--> 115 <220> FEATURE:
116 <223> OTHER INFORMATION:
W--> 117 <400> SEQUENCE: 5
C--> 118 caatgctagg tgtggtctgg ct 22
119 <210> SEQ ID NO: 6
120 <211> LENGTH: 22
121 <212> TYPE: DNA
122 <213> ORGANISM: Artificial Sequence
W--> 123 <220> FEATURE:
124 <223> OTHER INFORMATION:
W--> 125 <400> SEQUENCE: 6
C--> 126 gatctcaagt tgttgcacgt gc 22
127 <210> SEQ ID NO: 7
128 <211> LENGTH: 26
129 <212> TYPE: DNA
130 <213> ORGANISM: Artificial Sequence
W--> 131 <220> FEATURE:
132 <223> OTHER INFORMATION:
W--> 133 <400> SEQUENCE: 7
C--> 134 tggcagtcat cgtaggatca cccatg 26

VERIFICATION SUMMARY DATE: 09/12/2002
PATENT APPLICATION: **US/10/070,241** TIME: 16:06:00

Input Set : **A:\EP.txt**
Output Set: **N:\CRF4\09122002\J070241.raw**

L:4 M:283 W: Missing Blank Line separator, <120> field identifier
L:5 M:283 W: Missing Blank Line separator, <130> field identifier
L:6 M:270 C: Current Application Number differs, Replaced Current Application No
L:6 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:8 M:283 W: Missing Blank Line separator, <160> field identifier
L:9 M:283 W: Missing Blank Line separator, <210> field identifier
L:13 M:283 W: Missing Blank Line separator, <400> field identifier
L:72 M:283 W: Missing Blank Line separator, <400> field identifier
L:73 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=2
L:99 M:283 W: Missing Blank Line separator, <220> field identifier
L:101 M:283 W: Missing Blank Line separator, <400> field identifier
L:102 M:112 C: (48) String data converted to lower case,
L:107 M:283 W: Missing Blank Line separator, <220> field identifier
L:109 M:283 W: Missing Blank Line separator, <400> field identifier
L:110 M:112 C: (48) String data converted to lower case,
L:115 M:283 W: Missing Blank Line separator, <220> field identifier
L:117 M:283 W: Missing Blank Line separator, <400> field identifier
L:118 M:112 C: (48) String data converted to lower case,
L:123 M:283 W: Missing Blank Line separator, <220> field identifier
L:125 M:283 W: Missing Blank Line separator, <400> field identifier
L:126 M:112 C: (48) String data converted to lower case,
L:131 M:283 W: Missing Blank Line separator, <220> field identifier
L:133 M:283 W: Missing Blank Line separator, <400> field identifier
L:134 M:112 C: (48) String data converted to lower case,